

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:44:37 ; Search time 153 Seconds

(without alignments)
11.723 Million cell updates/sec

Title: HOLLY-9
Perfect score: 22
Sequence: 1 aaag 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	6	2	AAY42597 Human IgE
2	22	100.0	6	3	AAY85229 Human IgE
3	22	100.0	6	4	AAB82095 Hamster P
4	22	100.0	6	5	AAB15586 Hamster P
5	22	100.0	7	4	AAY69877 13C-label
6	22	100.0	7	4	AAB73728 Radiolabel
7	22	100.0	7	6	ADA38160 Peptide C
8	22	100.0	8	2	AAB89379 Beta-amy1
9	22	100.0	8	4	AAB82093 Hamster P
10	22	100.0	8	5	ABG71017 Prion pro
11	22	100.0	8	5	ABG05165 Prion pro
12	22	100.0	8	5	ABG15584 Hamster P
13	22	100.0	8	5	AAB26268 Human amy
14	22	100.0	8	7	ADD24684 Peptide a
15	22	100.0	8	8	ADJ64068 Human bet
16	22	100.0	9	2	AAW43905 Specific
17	22	100.0	9	5	ABG65845 Peptide 1
18	22	100.0	10	4	AAG84197 Arabidops
19	22	100.0	10	4	AAG84188 Human com
20	22	100.0	10	4	AAG97948 Human com
21	22	100.0	10	4	AAG97712 Human com
22	22	100.0	10	4	AAG97945 Human com
23	22	100.0	10	4	AAG97947 Human com
24	22	100.0	10	4	AAG97946 Human com
25	22	100.0	10	5	ABG65858 Peptide 1

26	22	100.0	10	5	ABG65874
27	22	100.0	11	6	ADA38149
28	22	100.0	11	6	ADA38151
29	22	100.0	11	6	AAO31161
30	22	100.0	11	6	AAO31163
31	22	100.0	11	7	ADC23466
32	22	100.0	11	7	ADC23468
33	22	100.0	11	7	ADD24690
34	22	100.0	11	7	ADD24689
35	22	100.0	12	2	AAW22038
36	22	100.0	12	2	AAW32561
37	22	100.0	12	4	ABG37466
38	22	100.0	12	4	ABG71386
39	22	100.0	12	6	ABU79022
40	22	100.0	12	6	ABW00156
41	22	100.0	12	7	ADE29207
42	22	100.0	12	8	ADH80963
43	22	100.0	12	8	ADH80962
44	22	100.0	12	8	ADL70328
45	22	100.0	12	8	ADL70310
46	22	100.0	12	8	ADL70316
47	22	100.0	12	8	ADL70325
48	22	100.0	12	8	ADL70313
49	22	100.0	12	8	ADL70319
50	22	100.0	12	8	ADL70322
51	22	100.0	12	8	ADN37740
52	22	100.0	13	3	AAV67844
53	22	100.0	13	5	ADG66555
54	22	100.0	13	5	ADG66553
55	22	100.0	13	5	ADG66552
56	22	100.0	13	5	ADG66556
57	22	100.0	13	5	ADG66554
58	22	100.0	13	6	AAO31195
59	22	100.0	13	7	ADC23477
60	22	100.0	13	7	ADC23476
61	22	100.0	14	2	AAW17680
62	22	100.0	14	2	AAW69817
63	22	100.0	14	2	AAW73743
64	22	100.0	14	2	AAW73853
65	22	100.0	14	2	AAU08208
66	22	100.0	14	6	ABU79033
67	22	100.0	14	6	ABP74859
68	22	100.0	14	6	ABP58083
69	22	100.0	14	7	ABW00167
70	22	100.0	15	5	ABE09749
71	22	100.0	16	2	AAW04447
72	22	100.0	16	2	AAW04483
73	22	100.0	16	4	ABU54074
74	22	100.0	16	7	ADL34426
75	22	100.0	17	4	AAW78078
76	22	100.0	17	5	ABG47084
77	22	100.0	17	8	ABO54338
78	22	100.0	18	2	AAW07530
79	22	100.0	18	2	AAW23360
80	22	100.0	18	2	AAW67021
81	22	100.0	18	3	AAW81054
82	22	100.0	18	3	ABG23279
83	22	100.0	18	7	ADG66316
84	22	100.0	18	8	ADO08751
85	22	100.0	19	2	AAW36792
86	22	100.0	19	2	AAW36794
87	22	100.0	19	2	AAW17681
88	22	100.0	19	6	ABP58082
89	22	100.0	19	6	ABU62604
90	22	100.0	19	8	ABO58531
91	22	100.0	20	2	AAW07528
92	22	100.0	20	2	AAW32319
93	22	100.0	20	3	AAW03085
94	22	100.0	20	4	AAW69493
95	22	100.0	20	4	AAW73061
96	22	100.0	20	4	AAE12262
97	22	100.0	20	5	AAE13243
98	22	100.0	20	5	AAE13243

ABG65874	Peptide 1
ADA38149	Peptide a
ADA38151	Control p
AAO31161	Prion (Pr
AAO31163	Prion (Pr
ADC23466	Peptide a
ADC23468	Peptide a
ADD24690	Peptide a
ADD24689	Peptide a
ADW22038	Antigenic
AAW32561	Prion tar
ABG37466	ATP-depen
ABU79022	Prion pro
ABW00156	Anti-Prp
ADE29207	Multivale
ADH80963	Peptide r
ADH80962	Peptide r
ADL70328	Peptide a
ADL70310	Peptide a
ADL70316	Peptide a
ADL70325	Peptide a
ADL70313	Peptide a
ADL70319	Peptide a
ADL70322	Peptide a
ADN37740	Hard segm
AAV67844	Alpha-2 a
ADG66555	B. subtil
ADG66553	B. subtil
ADG66552	B. subtil
ADG66556	B. subtil
ADG66554	B. subtil
AAO31195	Human bet
ADC23477	Peptide a
ADC23476	Peptide a
AAW17680	Prion pro
AAW69817	Peptide f
AAW73743	M. tuberc
AAW73853	M. tuberc
AAU08208	Mycobacte
ABU79033	Prion pro
ABP74859	Proteome
ABP58083	Human pri
ABW00167	Prion (Pr
ABE09749	Peptide f
AAW04447	Human imm
AAW04483	Human imm
ABU54074	Human DNA
ADL34426	MHC/HLA p
AAW78078	Human bon
ABG47084	Human pep
ABO54338	Human gen
AAW07530	B-cell ep
AAW23360	Human bet
AAW67021	Peptide M
AAW81054	Signal pe
ABG23279	Memordica
ADG66316	M. charan
ADO08751	Novel sur
AAW36792	Prion pro
AAW36794	Prion pro
AAW17681	Prion pro
ABP58082	Human pri
ABU62604	Hypotheri
ABO58531	Human gen
AAW07528	B-cell ep
AAW32319	Leishman
AAW03085	N-terminu
AAW69493	Synthetic
AAW73061	Machado-J
AAE12262	Mycobacte
AAE13243	Human pep

99	22	100.0	20	5	AAE13242	Aae13242 Human pep
100	22	100.0	20	5	AAE13235	Aae13235 Human lin
101	22	100.0	20	5	ADD93639	Add93639 Streptoco
102	22	100.0	20	7	ADD93661	Add93661 Streptoco
103	22	100.0	21	2	AAW53348	Aaw53348 Nephila c
104	22	100.0	21	3	AAW59072	Aaw59072 N. clavip
105	22	100.0	21	4	AAW59074	Aaw59074 Synthetic
106	22	100.0	21	4	AAW59107	Aaw59107 Human PrP
107	22	100.0	21	6	AAO16083	Aao16083 Mouse neu
108	22	100.0	21	6	AAO16080	Aao16080 Human neu
109	22	100.0	21	6	ABW82634	Abw82634 Human pri
110	22	100.0	21	6	ABU79034	Abu79034 Prion pro
111	22	100.0	21	7	ADC59529	Adc59529 Prion pep
112	22	100.0	21	7	ADC52086	Adc52086 Mouse pri
113	22	100.0	21	7	ABW00168	Abw00168 Prion (Pr
114	22	100.0	21	8	ADJ88131	Adj88131 Human PrP
115	22	100.0	21	8	ADJ88135	Adj88135 Mouse PrP
116	22	100.0	21	8	ADN00696	Adn00696 Human PrP
117	22	100.0	21	8	ADP44315	Adp44315 Chaperone
118	22	100.0	21	8	ADP44324	Adp44324 Chaperone
119	22	100.0	21	8	ADP44325	Adp44325 Chaperone
120	22	100.0	21	8	ADP44320	Adp44320 Chaperone
121	22	100.0	21	8	ADP44314	Adp44314 Chaperone
122	22	100.0	23	2	AAW76544	Aaw76544 HIV-1 TAT
123	22	100.0	23	2	AAW76550	Aaw76550 HIV-1 TAT
124	22	100.0	23	2	AAW76558	Aaw76558 HIV-1 TAT
125	22	100.0	23	2	AAW76552	Aaw76552 HIV-1 TAT
126	22	100.0	23	2	AAW76559	Aaw76559 HIV-1 TAT
127	22	100.0	23	3	AAW76559	Aaw76559 HIV-1 TAT
128	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
129	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
130	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
131	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
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139	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
140	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
141	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
142	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
143	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
144	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
145	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
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147	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
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149	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
150	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
151	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
152	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
153	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
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157	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
158	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
159	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
160	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
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162	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
163	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
164	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
165	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
166	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
167	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
168	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
169	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
170	22	100.0	23	4	AAW21563	Aaw21563 Peptide #
171	22	100.0	23	4	AAW21563	Aaw21563 Peptide #

ALIGNMENTS

RESULT 1

AAW42597	172	22	100.0	30	3	AAW59116	Aay59116 N. clavip
ID AAY42597 standard; peptide; 6 AA.	173	22	100.0	30	3	AAW59121	Aay59121 N. clavip
XX	174	22	100.0	30	3	AAW59124	Aay59124 N. clavip
AC	175	22	100.0	30	3	AAW59104	Aay59104 N. clavip
AC	176	22	100.0	30	3	AAW59123	Aay59123 N. clavip
DT	177	22	100.0	30	5	ABW79705	Abb79705 Extracell
DT	178	22	100.0	31	3	AAW59109	Aay59109 N. clavip
DE	179	22	100.0	31	3	AAW59111	Aay59111 Arabidops
DE	180	22	100.0	31	4	ABW38864	Abb38864 Peptide #
DE	181	22	100.0	31	4	ABW38864	Abb38864 Peptide #
DE	182	22	100.0	31	4	ABW38864	Abb38864 Peptide #
DE	183	22	100.0	31	4	ABW38864	Abb38864 Peptide #
DE	184	22	100.0	31	4	ABW38864	Abb38864 Peptide #
DE	185	22	100.0	31	4	ABW38864	Abb38864 Peptide #
DE	186	22	100.0	31	4	ABW38864	Abb38864 Peptide #
DE	187	22	100.0	31	5	ABW41891	Abb41891 Human liv
DE	188	22	100.0	31	7	ADD24215	Add24215 Human pri
DE	189	22	100.0	32	4	AAW59109	Aay59109 N. clavip
DE	190	22	100.0	32	4	AAW59107	Aay59107 N. clavip
DE	191	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
DE	192	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
DE	193	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
DE	194	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
DE	195	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
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DE	221	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
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DE	260	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
DE	261	22	100.0	32	2	AAW12613	Aar12613 HIV-1 p17
DE	262	22	100.0	32	2	AAW12613	Aar1261

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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:44:37 ; Search time 37 Seconds
(without alignments)
8.962 Million cell updates/sec

Title: HOLLY-9
Perfect score: 22
Sequence: 1 aaag 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 65318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Issued_Patents_AA.*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	6	2	US-08-232-539D-31
2	22	100.0	6	3	US-08-466-151-36
3	22	100.0	6	3	US-09-128-450-3
4	22	100.0	6	3	US-08-466-163B-36
5	22	100.0	6	3	US-09-823-494-3
6	22	100.0	6	4	US-09-802-096-36
7	22	100.0	6	4	US-09-802-077-36
8	22	100.0	7	2	US-08-442-461D-33
9	22	100.0	8	2	US-08-612-785B-17
10	22	100.0	8	3	US-09-128-450-1
11	22	100.0	8	3	US-08-617-267C-17
12	22	100.0	8	3	US-09-823-494-1
13	22	100.0	8	4	US-09-367-572-4
14	22	100.0	10	1	US-08-463-862-9
15	22	100.0	10	2	US-08-458-887-9
16	22	100.0	11	6	5178861-16
17	22	100.0	12	2	US-08-630-645-23
18	22	100.0	12	3	US-09-149-934-5
19	22	100.0	12	4	US-08-766-596A-23
20	22	100.0	12	5	PCT-US96-10220-23
21	22	100.0	14	1	US-08-556-823-3
22	22	100.0	14	1	US-08-556-823-4
23	22	100.0	14	4	US-08-766-596A-34
24	22	100.0	14	4	US-09-073-009-101
25	22	100.0	14	4	US-09-073-010-101
26	22	100.0	16	2	US-08-308-494A-2
27	22	100.0	18	1	US-08-240-712-33
28	22	100.0	22	28	Sequence 31, Appl
29	22	100.0	22	28	Sequence 36, Appl
30	22	100.0	22	28	Sequence 36, Appl
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35	22	100.0	22	28	Sequence 36, Appl
36	22	100.0	22	28	Sequence 36, Appl
37	22	100.0	22	28	Sequence 36, Appl
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98	22	100.0	22	28	Sequence 36, Appl
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100	22	100.0	22	28	Sequence 36, Appl

Sequence 33, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 5, Appl
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Sequence 12, Appl
Sequence 17, Appl
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Sequence 7, Appl
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Sequence 38, Appl
Sequence 6, Appl
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Sequence 20, Appl
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Sequence 22, Appl
Sequence 47, Appl
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Sequence 6, Appl
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Sequence 9, Appl
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Sequence 51, Appl
Sequence 2, Appl
Sequence 41, Appl
Sequence 48, Appl
Sequence 53, Appl
Sequence 58, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 41, Appl
Sequence 48, Appl
Sequence 53, Appl
Sequence 58, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 32, Appl
Sequence 75, Appl
Sequence 95, Appl
Sequence 46, Appl

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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:44:37 ; Search time 188 Seconds

(without alignments)
15.303 Million cell updates/sec

Title: HOLLY-9

Perfect score: 22

Sequence: 1 aaag 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	15	1 UN04 PINPS	P81673 pinus pinas
2	22	100.0	16	2 Q9Z0J2	Q9Z0J2 mus musculus
3	22	100.0	26	2 Q9UPD8	Q9UPD8 homo sapien
4	22	100.0	30	2 Q9QV43	Q9QV43 rattus sp.
5	22	100.0	33	2 Q6JUZ3	Q6JUZ3 ovis aries
6	22	100.0	33	2 Q6JUZ6	Q6JUZ6 ovis aries
7	22	100.0	33	2 AAQ81744	AAQ81744 ovis arie
8	22	100.0	33	2 AAQ81747	AAQ81747 ovis arie
9	22	100.0	34	2 Q9N1V1	Q9N1V1 equus caball
10	22	100.0	37	2 Q9XFN1	Q9XFN1 armoracia r
11	22	100.0	38	2 Q939W1	Q939W1 aeromonas s
12	22	100.0	39	2 Q90776	Q90776 gallus gall
13	22	100.0	40	2 P72435	P72435 streptomyce
14	22	100.0	43	2 Q7SEH1	Q7SEH1 neurospora
15	22	100.0	44	2 Q61736	Q61736 mus musculus
16	22	100.0	45	2 Q7RWY6	Q7RWY6 neurospora
17	22	100.0	45	2 Q7QW75	Q7QW75 anophelles g
18	22	100.0	45	2 Q7B303	Q7B303 paracoccus
19	22	100.0	47	2 Q7QXK7	Q7QXK7 giardia lam
20	22	100.0	51	2 Q6R517	Q6R517 brassica na
21	22	100.0	51	2 Q6ZGK6	Q6ZGK6 cryza sativ
22	22	100.0	51	2 Q7NFK6	Q7NFK6 chromobacte
23	22	100.0	51	2 AAQ00649	AAQ00649 brassica
24	22	100.0	51	2 BAD16926	BAD16926 cryza sat
25	22	100.0	52	2 Q8NQV4	Q8NQV4 corynebacte
26	22	100.0	52	2 CAF20017	CAF20017 corynebac
27	22	100.0	53	2 Q8RZF2	Q8RZF2 cryza sativ
28	22	100.0	53	2 Q8W083	Q8W083 cryza sativ
29	22	100.0	54	2 Q21846	Q21846 caenorhabdi
30	22	100.0	54	2 Q84487	Q84487 chlamydia t
31	22	100.0	54	2 Q92KT7	Q92KT7 rhizobium m

32	22	100.0	56	2 Q29163	Q29163 sus scrofa
33	22	100.0	57	2 Q08060	Q08060 zea mays (m
34	22	100.0	57	2 Q43474	Q43474 hordeum vul
35	22	100.0	57	2 Q9M7N1	Q9M7N1 triticum ae
36	22	100.0	57	2 Q94K78	Q94K78 arabidopsis
37	22	100.0	57	2 Q8U712	Q8U712 agrobacteri
38	22	100.0	60	1 SERL_DROME	Q9V62 drosophila
39	22	100.0	60	1 UR1_PLAFA	P21624 platichthys
40	22	100.0	60	2 Q92057	Q92057 gallus gall
41	22	100.0	61	2 Q6H511	Q6H511 cryza sativ
42	22	100.0	62	2 Q87587	Q87587 rhizobium l
43	22	100.0	62	2 P87087	P87087 candida dub
44	22	100.0	62	2 Q6YS23	Q6YS23 cryza sativ
45	22	100.0	62	2 Q7XV66	Q7XV66 cryza sativ
46	22	100.0	62	2 BAC84747	BAC84747 cryza sat
47	22	100.0	63	2 P87088	P87088 candida dub
48	22	100.0	63	2 Q6NNY1	Q6NNY1 drosophila
49	22	100.0	63	2 Q6K1Q4	Q6K1Q4 cryza sativ
50	22	100.0	63	2 Q7XGR8	Q7XGR8 cryza sativ
51	22	100.0	63	2 Q8W2R9	Q8W2R9 cryza sativ
52	22	100.0	63	2 AAR82819	AAR82819 drosophil
53	22	100.0	63	2 BAD21555	BAD21555 cryza sat
54	22	100.0	63	2 BAD22519	BAD22519 cryza sat
55	22	100.0	64	2 Q6ETB2	Q6ETB2 cryza sativ
56	22	100.0	66	1 KIN2_ARATH	P31169 arabidopsis
57	22	100.0	66	1 RL35_BRUME	Q8Y670 brucella me
58	22	100.0	66	2 Q5H9N7	Q5H9N7 yarrowia li
59	22	100.0	66	2 Q6CB08	Q6CB08 yarrowia li
60	22	100.0	66	2 Q94E92	Q94E92 cryza sativ
61	22	100.0	66	2 Q7VCF8	Q7VCF8 prochloroco
62	22	100.0	66	2 AAM47864	AAM47864 arabidops
63	22	100.0	66	2 AAL61909	AAL61909 arabidops
64	22	100.0	67	1 RL35_AGR75	Q8Uin8 agrobacteri
65	22	100.0	67	1 RL35_RHIME	Q92st2 rhizobium m
66	22	100.0	67	2 Q7Y1Q7	Q7Y1Q7 zea mays (m
67	22	100.0	67	2 Q7Y1S6	Q7Y1S6 zea mays (m
68	22	100.0	67	2 Q6H5B6	Q6H5B6 cryza sativ
69	22	100.0	67	2 Q8GZ21	Q8GZ21 cryza sativ
70	22	100.0	68	2 Q6L587	Q6L587 cryza sativ
71	22	100.0	68	2 Q8H877	Q8H877 cryza sativ
72	22	100.0	68	2 AAT38020	AAT38020 cryza sat
73	22	100.0	70	1 RPCX_YEAST	P04022 saccharomyc
74	22	100.0	70	2 Q754P6	Q754P6 ashbya goes
75	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
76	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
77	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
78	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
79	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
80	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
81	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
82	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
83	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
84	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
85	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
86	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
87	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
88	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
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90	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
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92	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
93	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
94	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
95	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
96	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
97	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
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103	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc
104	22	100.0	70	2 Q6CRL9	Q6CRL9 kluyveromyc

105	22	100.0	71	2	CAD98988	Cad98988 enterobac
106	22	100.0	71	2	CAD98989	Cad98989 enterobac
107	22	100.0	71	2	CAD98990	Cad98990 enterobac
108	22	100.0	71	2	CAD98991	Cad98991 enterobac
109	22	100.0	71	2	CAD98992	Cad98992 enterobac
110	22	100.0	71	2	CAD98993	Cad98993 enterobac
111	22	100.0	71	2	CAD98994	Cad98994 enterobac
112	22	100.0	71	2	CAD98995	Cad98995 enterobac
113	22	100.0	71	2	CAD98996	Cad98996 enterobac
114	22	100.0	71	2	CAD98997	Cad98997 enterobac
115	22	100.0	73	2	Q62K19	Q62K19 oryza sativ
116	22	100.0	73	2	BAD08891	BAD08891 oryza sativ
117	22	100.0	74	2	Q8H5U5	Q8H5U5 oryza sativ
118	22	100.0	74	2	Q94E83	Q94E83 oryza sativ
119	22	100.0	75	2	Q9V2Y1	Q9V2Y1 oryza sativ
120	22	100.0	75	2	Q8N0Z1	Q8N0Z1 methanobact
121	22	100.0	76	2	Q27310	Q27310 methanobact
122	22	100.0	76	2	Q62710	Q62710 oryza sativ
123	22	100.0	76	2	Q75KL3	Q75KL3 oryza sativ
124	22	100.0	76	2	Q7XIW3	Q7XIW3 oryza sativ
125	22	100.0	76	2	Q84XF0	Q84XF0 oryza sativ
126	22	100.0	76	2	Q84XP7	Q84XP7 oryza sativ
127	22	100.0	76	2	Q8S0E6	Q8S0E6 oryza sativ
128	22	100.0	76	2	BAD07961	BAD07961 oryza sativ
129	22	100.0	76	2	AAS98441	AAS98441 oryza sativ
130	22	100.0	77	2	Q8LRA5	Q8LRA5 oryza sativ
131	22	100.0	77	2	Q9XIX4	Q9XIX4 oryza sativ
132	22	100.0	77	2	Q7TVE8	Q7TVE8 mycobacteri
133	22	100.0	77	2	Q7D4N3	Q7D4N3 mycobacteri
134	22	100.0	77	2	Q9WSA4	Q9WSA4 human immun
135	22	100.0	77	2	CAE55650	CAE55650 mycobacte
136	22	100.0	78	1	PUR9_CHRVI	PUR9_CHRVI
137	22	100.0	78	2	Q6BU54	Q6BU54 debaromyce
138	22	100.0	78	2	Q8LNB9	Q8LNB9 oryza sativ
139	22	100.0	80	2	Q8N160	Q8N160 homo sapien
140	22	100.0	80	2	Q6L5I8	Q6L5I8 oryza sativ
141	22	100.0	80	2	Q9WM18	Q9WM18 pseudomonas
142	22	100.0	80	2	Q98N11	Q98N11 rhizobium l
143	22	100.0	80	2	AAT39211	AAT39211 oryza sativ
144	22	100.0	81	2	Q61GY1	Q61GY1 drosophila
145	22	100.0	81	2	Q96796	Q96796 skeletonema
146	22	100.0	81	2	Q84SW6	Q84SW6 oryza sativ
147	22	100.0	81	2	Q9M4Y6	Q9M4Y6 oryza sativ
148	22	100.0	81	2	Q9WSA1	Q9WSA1 human immun
149	22	100.0	82	2	P93427	P93427 oryza sativ
150	22	100.0	82	2	Q6D780	Q6D780 erwinia car
151	22	100.0	83	2	Q6K4B4	Q6K4B4 oryza sativ
152	22	100.0	83	2	Q6Z606	Q6Z606 oryza sativ
153	22	100.0	83	2	Q84P08	Q84P08 oryza sativ
154	22	100.0	83	2	Q6TV92	Q6TV92 bovine papu
155	22	100.0	83	2	BAC99677	BAC99677 oryza sativ
156	22	100.0	83	2	AAR98453	AAR98453 bovine pa
157	22	100.0	83	2	BAD22255	BAD22255 oryza sativ
158	22	100.0	84	2	Q9NTR9	Q9NTR9 homo sapien
159	22	100.0	84	2	Q7PNA9	Q7PNA9 anopheles g
160	22	100.0	84	2	Q64827	Q64827 human adeno
161	22	100.0	84	2	Q8QS40	Q8QS40 chimpanzee
162	22	100.0	85	1	MRKD_RAT	MRKD_RAT
163	22	100.0	85	2	Q6H724	Q6H724 rattus norv
164	22	100.0	85	2	Q8XW06	Q8XW06 oryza sativ
165	22	100.0	86	1	YBIJ_ECOLI	YBIJ_ECOLI
166	22	100.0	86	2	Q7XVE5	Q7XVE5 oryza sativ
167	22	100.0	86	2	Q6H751	Q6H751 oryza sativ
168	22	100.0	86	2	Q9FTX8	Q9FTX8 oryza sativ
169	22	100.0	86	2	Q6EN67	Q6EN67 oryza sativ
170	22	100.0	86	2	Q7AGC3	Q7AGC3 escherichia
171	22	100.0	86	2	Q8G2Q4	Q8G2Q4 brucella su
172	22	100.0	86	2	Q8X7X2	Q8X7X2 escherichia
173	22	100.0	86	2	Q8XFN7	Q8XFN7 salmonella
174	22	100.0	86	2	Q8YF68	Q8YF68 brucella me
175	22	100.0	86	2	Q7CQW3	Q7CQW3 salmonella
176	22	100.0	87	2	Q6YX56	Q6YX56 oryza sativ
177	22	100.0	87	2	Q6Z3Q2	Q6Z3Q2 oryza sativ
178	22	100.0	87	2	Q6ZTQ5	Q6ZTQ5 oryza sativ
179	22	100.0	87	2	Q93VJ3	Q93VJ3 oryza sativ
180	22	100.0	87	2	BAC84116	BAC84116 oryza sativ
181	22	100.0	87	2	BAD03847	BAD03847 oryza sativ
182	22	100.0	87	2	BAD05241	BAD05241 oryza sativ
183	22	100.0	88	1	RS20_STRCO	RS20_STRCO
184	22	100.0	88	2	P91335	P91335 streptomyce
185	22	100.0	88	2	Q7XVI7	Q7XVI7 oryza sativ
186	22	100.0	88	2	Q7YIS2	Q7YIS2 zea mays (m
187	22	100.0	88	2	Q7YIS4	Q7YIS4 zea mays (m
188	22	100.0	88	2	Q6H4D7	Q6H4D7 oryza sativ
189	22	100.0	88	2	Q9LIX6	Q9LIX6 oryza sativ
190	22	100.0	88	2	Q8ZBZ4	Q8ZBZ4 streptomyce
191	22	100.0	88	2	Q92RU0	Q92RU0 rhizobium m
192	22	100.0	89	2	Q9N9Q1	Q9N9Q1 leishmania
193	22	100.0	89	2	Q84Z20	Q84Z20 oryza sativ
194	22	100.0	89	2	Q73SS2	Q73SS2 mycobacteri
195	22	100.0	89	2	Q6FB75	Q6FB75 acinetobact
196	22	100.0	89	2	Q709T8	Q709T8 human immun
197	22	100.0	89	2	AAS06551	AAS06551 mycobacte
198	22	100.0	89	2	CAE54783	CAE54783 human imm
199	22	100.0	90	2	Q7S7Q0	Q7S7Q0 neurospora
200	22	100.0	90	2	Q8H4N9	Q8H4N9 oryza sativ

ALIGNMENTS

RESULT 1

UN04_PINPS STANDARD; PRT; 15 AA.
 AC P81673;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of needles (N143) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Fahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- INDUCTION: By water stress.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.2, its MW is: 21 kDa.
 KW Direct protein sequencing.
 FT NON_TER 1 15
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1489 MW; CE4D85E99308227A CRC64;

Query Match 100.0%; Score 22; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAG 5
 Db 7 AAAAG 11

RESULT 2

Q9Z0J2 PRELIMINARY; PRT; 16 AA.
 AC Q9Z0J2;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:44:37 ; Search time 39 Seconds

(without alignments)
12.335 Million cell updates/sec

Title: HOLLY-9

Perfect score: 22

Sequence: 1 aaaag 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

PIR-79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	19	2 B43978	urotensin I precu
2	22	100.0	35	2 A61375	basic fibroblast g
3	22	100.0	54	2 E70787	hypothetical glyci
4	22	100.0	54	2 C71570	hypothetical prote
5	22	100.0	54	2 T29665	hypothetical prote
6	22	100.0	57	2 T03654	glyceraldehyde-3-p
7	22	100.0	57	2 AG3105	conserved hypothet
8	22	100.0	66	2 AB3503	LSU ribosomal prot
9	22	100.0	66	2 S22529	cold-regulated pro
10	22	100.0	67	2 F97389	SOS ribosomal prot
11	22	100.0	67	2 AG2607	SOS ribosomal prot
12	22	100.0	70	2 S58932	DNA-directed RNA p
13	22	100.0	74	2 T47211	cag-6 protein [imp
14	22	100.0	76	2 A69033	hypothetical prote
15	22	100.0	77	2 F70598	probable PE protei
16	22	100.0	86	2 AD0600	probable exported
17	22	100.0	86	2 B64817	vblj protein precu
18	22	100.0	86	2 B85589	hypothetical prote
19	22	100.0	86	2 H90738	hypothetical prote
20	22	100.0	86	2 AC3459	hypothetical prote
21	22	100.0	88	2 T34429	hypothetical prote
22	22	100.0	90	2 JN0492	hypothetical 9.7K
23	22	100.0	92	1 RIPS	somatostatin I pre
24	22	100.0	92	2 B87456	ribosomal protein
25	22	100.0	93	2 C82650	hypothetical prote
26	22	100.0	97	2 T30458	hypothetical prote
27	22	100.0	98	2 B70568	probable PE protei
28	22	100.0	98	2 D75519	hypothetical prote
29	22	100.0	99	1 R6MXL2	ribosomal protein

30	22	100.0	99	2 A70930	probable PE protei
31	22	100.0	99	2 F70929	probable PE protei
32	22	100.0	100	2 S20482	hypothetical prote
33	22	100.0	101	2 A33351	H+-transporting tw
34	22	100.0	102	2 D90203	ATP synthase subun
35	22	100.0	104	2 S45400	probable membrane
36	22	100.0	104	2 F83370	hydrogen cyanide s
37	22	100.0	106	1 R8BY2B	acidic ribosomal p
38	22	100.0	106	2 TS2147	ribosomal protein
39	22	100.0	109	2 T04144	DNA binding protei
40	22	100.0	110	1 R6BY22	60S acidic ribosom
41	22	100.0	110	1 R6BYP3	60S acidic ribosom
42	22	100.0	110	2 JC2260	Streptovorticillin
43	22	100.0	111	1 R8S512	ribosomal protein
44	22	100.0	111	2 S43115	acidic ribosomal p
45	22	100.0	111	2 S41866	acidic ribosomal p
46	22	100.0	111	2 D75566	conserved hypothet
47	22	100.0	111	2 E98181	hypothetical prote
48	22	100.0	112	1 R6UT2B	acidic ribosomal p
49	22	100.0	112	2 S35440	acidic ribosomal p
50	22	100.0	112	2 T36440	hypothetical prote
51	22	100.0	113	1 R6FFP2	acidic ribosomal p
52	22	100.0	113	2 S43109	acidic ribosomal p
53	22	100.0	113	2 T30041	hypothetical prote
54	22	100.0	113	2 T22851	hypothetical prote
55	22	100.0	115	2 G87300	dihydroneopterin a
56	22	100.0	116	1 A28968	somatostatin I pre
57	22	100.0	116	1 RIBOS1	somatostatin I pre
58	22	100.0	116	1 RIHUS1	somatostatin I pre
59	22	100.0	116	1 S20630	somatostatin precu
60	22	100.0	116	1 IPAF	insulin precursor
61	22	100.0	117	2 H84651	hypothetical prote
62	22	100.0	119	2 T36513	hypothetical prote
63	22	100.0	120	2 PH0083	neuroglian, long c
64	22	100.0	121	2 D86783	SOS ribosomal prot
65	22	100.0	123	2 A34172	traj protein - Esc
66	22	100.0	124	2 H81005	adhesin complex pr
67	22	100.0	126	2 T16727	hypothetical prote
68	22	100.0	129	2 T31200	hypothetical prote
69	22	100.0	129	2 T00003	peph protein - Aci
70	22	100.0	130	2 S41571	blastocidin-S deam
71	22	100.0	130	2 H81684	ribosomal protein
72	22	100.0	130	2 A71530	ribosomal protein
73	22	100.0	132	1 MTON1K	melanin-concentrat
74	22	100.0	132	1 MTON2K	melanin-concentrat
75	22	100.0	132	2 S34654	melanin-concentrat
76	22	100.0	132	2 S34653	melanin-concentrat
77	22	100.0	132	2 A32910	melanin-concentrat
78	22	100.0	132	2 B32910	melanin-concentrat
79	22	100.0	132	2 B85092	hypothetical prote
80	22	100.0	132	2 S43488	homeotic protein L
81	22	100.0	134	2 A26986	hypothetical prote
82	22	100.0	134	2 C82030	probable cytochrom
83	22	100.0	135	2 F87264	MAPEG family prote
84	22	100.0	135	2 G72601	hypothetical prote
85	22	100.0	136	2 A82388	hypothetical prote
86	22	100.0	136	2 D82982	cytochrome c5 PA33
87	22	100.0	137	2 H84218	hypothetical prote
88	22	100.0	138	2 S13332	hypothetical prote
89	22	100.0	138	2 C87389	hypothetical prote
90	22	100.0	139	2 A81938	probable membrane
91	22	100.0	140	2 C71326	probable V-type AT
92	22	100.0	141	2 C83007	probable transcrip
93	22	100.0	142	2 E95263	hypothetical prote
94	22	100.0	143	2 S05543	dehydrin 9 - barle
95	22	100.0	144	2 D72517	hypothetical prote
96	22	100.0	145	2 H87436	hypothetical prote
97	22	100.0	146	2 T10511	hypothetical prote
98	22	100.0	147	2 H72548	hypothetical prote
99	22	100.0	150	2 S69530	hypothetical prote
100	22	100.0	151	2 S70787	curlin nucleator p
101	22	100.0	151	2 G90806	minor curlin subun
102	22	100.0	151	2 G85665	curlin minor chain

103 22 100.0 151 2 H87407 conserved hypothet
 104 22 100.0 151 2 E70615 hypothetical prote
 105 22 100.0 153 2 T43895 oleosin-like prote
 106 22 100.0 153 2 T03463 hypothetical prote
 107 22 100.0 155 2 T21364 hypothetical prote
 108 22 100.0 157 2 T02034 early light-induce
 109 22 100.0 157 2 T33892 hypothetical prote
 110 22 100.0 157 2 C70882 hypothetical prote
 111 22 100.0 157 2 T33329 probable DNA-bind
 112 22 100.0 158 2 H75028 probable H+-transp
 113 22 100.0 158 2 S35787 US9 protein - bovi
 114 22 100.0 162 2 P06614 superoxide dismuta
 115 22 100.0 162 2 T45343 hypothetical prote
 116 22 100.0 162 2 D71214 hypothetical prote
 117 22 100.0 165 2 H75471 fimbriata-associat
 118 22 100.0 165 2 T17031 hypothetical prote
 119 22 100.0 166 2 T0746 hypothetical prote
 120 22 100.0 166 2 AD3624 hypothetical prote
 121 22 100.0 166 2 A45119 basic helix-loop-h
 122 22 100.0 167 2 T04903 iron-sulfur cofact
 123 22 100.0 167 2 A55438 transcription fact
 124 22 100.0 168 2 T02036 early light-induce
 125 22 100.0 168 2 S72171 helix-loop-helix p
 126 22 100.0 168 2 G70587 hypothetical prote
 127 22 100.0 169 2 H84191 hypothetical prote
 128 22 100.0 170 2 F81038 probable shikimate
 129 22 100.0 172 2 T51122 crk protein, limpo
 130 22 100.0 173 2 T51469 glycine/proline-ri
 131 22 100.0 174 2 T02869 globulin 1 precurs
 132 22 100.0 174 2 F84338 hypothetical prote
 133 22 100.0 175 2 S72704 Lepb1170 C2 203 pr
 134 22 100.0 176 2 I48752 gene RXRbeta1 prot
 135 22 100.0 176 2 A34690 DNA-binding protei
 136 22 100.0 176 2 AF0460 probable membrane
 137 22 100.0 177 2 I49069 A+U-rich RNA-bind
 138 22 100.0 178 2 G87307 hypothetical prote
 139 22 100.0 178 2 E70069 hypothetical prote
 140 22 100.0 178 2 T06094 hypothetical prote
 141 22 100.0 178 2 E75340 conserved hypothet
 142 22 100.0 178 2 E88637 protein W09G12.6 [c
 143 22 100.0 179 2 G75594 cobinamide kinase/
 144 22 100.0 179 2 T35750 hypothetical prote
 145 22 100.0 180 2 C61600 segmentation prote
 146 22 100.0 180 2 T25598 hypothetical prote
 147 22 100.0 180 2 S05616 chorion protein si
 148 22 100.0 180 2 UC7876 prion protein homo
 149 22 100.0 182 2 F70586 hypothetical prote
 150 22 100.0 183 2 T02974 probable DNA bind
 151 22 100.0 184 2 S57778 oleosin 1 - barley
 152 22 100.0 184 2 D87605 transcription regu
 153 22 100.0 185 2 G72783 hypothetical prote
 154 22 100.0 186 2 D83344 hypothetical prote
 155 22 100.0 186 2 C82029 probable adhesin c
 156 22 100.0 186 2 T35736 hypothetical prote
 157 22 100.0 187 2 S49755 adenine phosphorib
 158 22 100.0 188 2 A34014 integrin alpha-3 c
 159 22 100.0 189 2 A48834 basic fibroblast g
 160 22 100.0 189 2 G69932 hypothetical prote
 161 22 100.0 190 2 E70840 probable dehydrata
 162 22 100.0 191 2 H83151 hypothetical prote
 163 22 100.0 193 2 B87460 phosphoribosylglyc
 164 22 100.0 193 2 T36959 hypothetical prote
 165 22 100.0 193 2 A70583 probable resolvase
 166 22 100.0 194 2 H70672 probable resolvase
 167 22 100.0 195 2 T28653 resolvase - pseudo
 168 22 100.0 195 2 S42228 BHV-1 protein homo
 169 22 100.0 195 2 A82201 cytochrome b-245 a
 170 22 100.0 195 2 H95297 probable allantoin
 171 22 100.0 196 2 E83895 transcription regu
 172 22 100.0 197 2 S26493 translation initia
 173 22 100.0 198 2 F84264 sulfite oxidase ho
 174 22 100.0 198 2 C32998 chorion protein S1
 175 22 100.0 199 2 T49450 hypothetical prote

176 22 100.0 200 2 B71295 probable cell divi
 177 22 100.0 201 2 E84189 hypothetical prote
 178 22 100.0 202 2 B87340 transcription regu
 179 22 100.0 203 1 TVHUC2 GTP-binding protei
 180 22 100.0 203 2 D81116 RNA methyltransfer
 181 22 100.0 204 2 T35012 probable transcrip
 182 22 100.0 204 2 H70648 probable regulator
 183 22 100.0 204 2 G84530 probable RING-H2 z
 184 22 100.0 205 2 B87609 hypothetical prote
 185 22 100.0 205 2 F84274 halocyanin precurs
 186 22 100.0 206 2 G83854 hypothetical prote
 187 22 100.0 206 2 S76279 hypothetical prote
 188 22 100.0 207 2 AC2950 transcription regu
 189 22 100.0 207 2 G87507 glutathione S-tran
 190 22 100.0 208 2 D75556 phosphoribosylanth
 191 22 100.0 208 2 G81169 N-(5'-phosphoribos
 192 22 100.0 208 2 T30625 hypothetical prote
 193 22 100.0 208 2 E86221 hypothetical prote
 194 22 100.0 209 2 H75626 DNA-binding respon
 195 22 100.0 209 2 G69321 conserved hypothet
 196 22 100.0 210 2 E86976 probable guanilate
 197 22 100.0 210 2 F70546 hypothetical prote
 198 22 100.0 210 2 D97502 hypothetical prote
 199 22 100.0 210 2 AH2720 RhtB family transp
 200 22 100.0 210 2 H70687 hypothetical prote

ALIGNMENTS

RESULT 1

utotensin I precursor - European flounder (fragment)

C:Species: Platichthys flesus (European flounder)

C:Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 18-Jun-1993

C:Accession: B43978

R:Conlon, J.M.; Arnold-Reed, D.E.; Balment, R.J.

Peptides 11, 891-895, 1990

A:Title: Utotensin I and its N-terminal flanking peptide from the flounder, Platichthys

A:Reference number: A43978

A:Accession: B43978

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <CON>

Query Match 100.0%; Score 22; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 AAAG 5

Db

1 AAAG 5

RESULT 2

A61375

basic fibroblast growth factor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994

C:Accession: A61375

R:Powell, P.P.; Klagsbrun, M.

J. Cell. Physiol. 148, 202-210, 1991

A:Title: Three forms of rat basic fibroblast growth factor are made from a single mRNA

A:Reference number: A61375; MUID:91349212; PMID:1880150

A:Accession: A61375

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-35 <POW>

C:Genetics:

A:Start codon: AGG

C:Keywords: alternative initiators

Query Match 100.0%; Score 22; DB 2; Length 35;

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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:44:37 ; Search time 777 Seconds
(without alignments)
2.282 Million cell updates/sec

Title: HOLLY-9
Perfect score: 22
Sequence: 1 aaag 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	22	100.0	6 9	US-09-802-077-36
2	22	100.0	6 9	US-09-802-096-36
3	22	100.0	6 9	US-09-823-494-3
4	22	100.0	6 10	US-09-925-179-36
5	22	100.0	7 15	US-10-294-114A-23
6	22	100.0	8 9	US-09-823-494-1
7	22	100.0	8 9	US-09-972-475-17
8	22	100.0	8 9	US-09-996-357-4
9	22	100.0	8 15	US-10-463-729-17
10	22	100.0	9 8	US-08-821-739A-109
11	22	100.0	10 10	US-09-572-404B-3907
12	22	100.0	10 10	US-09-572-404B-4140
13	22	100.0	10 10	US-09-572-404B-4141

14	22	100.0	10	US-09-572-404B-4142	Sequence 4142, Ap
15	22	100.0	10	US-09-572-404B-4143	Sequence 4143, Ap
16	22	100.0	10	US-09-572-270A-828	Sequence 828, App
17	22	100.0	10	US-09-572-270A-837	Sequence 837, App
18	22	100.0	11	US-10-368-517-11	Sequence 11, Appl
19	22	100.0	11	US-10-368-517-12	Sequence 12, Appl
20	22	100.0	11	US-10-368-517-14	Sequence 14, Appl
21	22	100.0	11	US-10-368-517-15	Sequence 15, Appl
22	22	100.0	11	US-10-368-517-24	Sequence 24, Appl
23	22	100.0	11	US-10-368-517-25	Sequence 25, Appl
24	22	100.0	11	US-10-368-517-38	Sequence 38, Appl
25	22	100.0	11	US-10-368-517-39	Sequence 39, Appl
26	22	100.0	11	US-10-294-114A-9	Sequence 9, Appli
27	22	100.0	11	US-10-294-114A-10	Sequence 10, Appl
28	22	100.0	11	US-10-294-114A-12	Sequence 12, Appl
29	22	100.0	11	US-10-294-114A-13	Sequence 13, Appl
30	22	100.0	12	US-09-077-439A-10	Sequence 10, Appl
31	22	100.0	12	US-10-235-483-23	Sequence 23, Appl
32	22	100.0	12	US-10-368-517-42	Sequence 42, Appl
33	22	100.0	12	US-10-685-105-9	Sequence 9, Appli
34	22	100.0	13	US-10-368-517-30	Sequence 30, Appl
35	22	100.0	13	US-10-368-517-31	Sequence 31, Appl
36	22	100.0	13	US-10-468-496-1044	Sequence 1044, Ap
37	22	100.0	13	US-10-468-496-1045	Sequence 1045, Ap
38	22	100.0	13	US-10-468-496-1046	Sequence 1046, Ap
39	22	100.0	13	US-10-468-496-1047	Sequence 1047, Ap
40	22	100.0	13	US-10-468-496-1048	Sequence 1048, Ap
41	22	100.0	14	US-09-073-009-101	Sequence 101, App
42	22	100.0	14	US-09-793-306-101	Sequence 101, App
43	22	100.0	14	US-10-235-483-34	Sequence 34, Appl
44	22	100.0	14	US-10-394-980-142	Sequence 142, App
45	22	100.0	14	US-09-864-761-48307	Sequence 48307, A
46	22	100.0	17	US-10-029-386-27972	Sequence 27972, A
47	22	100.0	18	US-10-101-952-1	Sequence 1, Appli
48	22	100.0	19	US-10-029-386-32165	Sequence 32165, A
49	22	100.0	19	US-10-116-061-3	Sequence 3, Appli
50	22	100.0	19	US-10-116-061-5	Sequence 5, Appli
51	22	100.0	20	US-09-813-333-47	Sequence 47, Appl
52	22	100.0	20	US-10-100-312-12	Sequence 12, Appl
53	22	100.0	20	US-10-044-703-47	Sequence 47, Appl
54	22	100.0	20	US-10-239-103-47	Sequence 47, Appl
55	22	100.0	20	US-10-240-430-3	Sequence 3, Appli
56	22	100.0	20	US-10-240-430-10	Sequence 10, Appl
57	22	100.0	20	US-10-240-430-11	Sequence 11, Appl
58	22	100.0	20	US-10-383-930-19	Sequence 19, Appl
59	22	100.0	20	US-10-383-930-41	Sequence 41, Appl
60	22	100.0	20	US-10-738-443-93	Sequence 93, Appl
61	22	100.0	21	US-09-808-037-25	Sequence 25, Appl
62	22	100.0	21	US-09-808-037-29	Sequence 29, Appl
63	22	100.0	21	US-10-162-889-25	Sequence 25, Appl
64	22	100.0	21	US-10-162-889-29	Sequence 29, Appl
65	22	100.0	21	US-10-235-483-35	Sequence 35, Appl
66	22	100.0	21	US-10-384-788-25	Sequence 25, Appl
67	22	100.0	21	US-10-384-788-29	Sequence 29, Appl
68	22	100.0	21	US-10-461-864-1	Sequence 1, Appli
69	22	100.0	21	US-10-738-443-94	Sequence 94, Appl
70	22	100.0	23	US-09-823-494-7	Sequence 7, Appli
71	22	100.0	23	US-09-864-761-42131	Sequence 42131, A
72	22	100.0	23	US-09-813-333-58	Sequence 58, Appl
73	22	100.0	23	US-10-044-703-58	Sequence 58, Appl
74	22	100.0	23	US-10-239-103-58	Sequence 58, Appl
75	22	100.0	27	US-09-823-494-10	Sequence 10, Appl
76	22	100.0	27	US-09-855-604-658	Sequence 658, App
77	22	100.0	27	US-10-357-322-11	Sequence 11, Appl
78	22	100.0	27	US-10-412-672-11	Sequence 11, Appl
79	22	100.0	27	US-10-789-102-75	Sequence 75, Appl
80	22	100.0	29	US-09-823-494-9	Sequence 9, Appli
81	22	100.0	29	US-09-864-761-44850	Sequence 44850, A
82	22	100.0	29	US-10-116-061-51	Sequence 51, Appl
83	22	100.0	30	US-10-412-672-13	Sequence 13, Appl
84	22	100.0	31	US-09-864-761-39166	Sequence 39166, A
85	22	100.0	33	US-09-823-494-8	Sequence 8, Appli
86	22	100.0	33	US-09-823-494-17	Sequence 17, Appl

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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:57:53 ; Search time 66 Seconds
(without alignments)
27.176 Million cell updates/sec

Title: HOLLY-13

Perfect score: 17

Sequence: 1 xlaaa 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : A_Geneseq_23Sep04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	6	5	Aae20126 Human TRI
2	17	100.0	6	6	Abu07730 Human leu
3	17	100.0	7	3	Aay67945 Vector pe
4	17	100.0	7	5	Abg60561 Selective
5	17	100.0	7	5	Aau75591 pET22b ve
6	17	100.0	7	6	Aao26947 Tumour ta
7	17	100.0	7	6	Ada20229 Peptide S
8	17	100.0	7	7	Adf53385 Adeno-as
9	17	100.0	8	2	Aar33326 IGE Kabat
10	17	100.0	8	2	Aay42609 Human IGE
11	17	100.0	8	3	Aay85218 Human IGE
12	17	100.0	8	3	Aay85251 Human IGE
13	17	100.0	8	3	Aay69117 Subsequen
14	17	100.0	8	3	Aay69109 Subsequen
15	17	100.0	8	3	Aay69112 Subsequen
16	17	100.0	8	3	Aay69110 Subsequen
17	17	100.0	8	3	Aay69111 Subsequen
18	17	100.0	8	3	Aay69113 Subsequen
19	17	100.0	8	3	Aay69114 Subsequen
20	17	100.0	8	3	Aay69116 Subsequen
21	17	100.0	8	3	Aay69115 Subsequen
22	17	100.0	8	3	Aay69130 Subsequen
23	17	100.0	8	3	Aay69141 Peptidomi
24	17	100.0	8	3	Aay69932 Human cyc
25	17	100.0	9	2	Aar66567 Cyclic gu

26	17	100.0	9	2	AAW00691 Positive
27	17	100.0	9	2	AAW04637 Null pept
28	17	100.0	9	2	AAW46647 Immunogen
29	17	100.0	9	2	AAW14988 Bovine CG
30	17	100.0	9	5	ABP97067 Human tum
31	17	100.0	9	6	ABP58411 Null pept
32	17	100.0	9	6	ABP09615 Human can
33	17	100.0	9	6	ABR09804 Human can
34	17	100.0	9	6	ABR09415 Human can
35	17	100.0	9	6	ABR09386 Human can
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39	17	100.0	9	6	ABR09188 Human can
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41	17	100.0	9	6	ABR09813 Human can
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45	17	100.0	9	6	ABR10218 Human can
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57	17	100.0	9	6	ABR10002 Human can
58	17	100.0	9	6	ABR10210 Human can
59	17	100.0	9	6	ABR08993 Human can
60	17	100.0	9	6	ABR09993 Human can
61	17	100.0	9	6	ABR10173 Human can
62	17	100.0	9	6	ABR09604 Human can
63	17	100.0	9	6	ABR09616 Human can
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66	17	100.0	9	6	ABR10031 Human can
67	17	100.0	9	6	ABP96451 HLA class
68	17	100.0	9	6	ABP96453 HLA class
69	17	100.0	9	6	ABP96478 HLA class
70	17	100.0	9	6	ABP96477 HLA class
71	17	100.0	9	6	ABU63174 CGB-PDB P
72	17	100.0	9	7	ABU64355 Human AAC
73	17	100.0	9	7	ADI15709 HLA-A2 re
74	17	100.0	9	7	ADK23708 Human 98P
75	17	100.0	9	7	ADK24375 Human 98P
76	17	100.0	9	7	ADK23721 Human 98P
77	17	100.0	9	7	ADK24381 Human 98P
78	17	100.0	9	8	ADK23565 Human IFN
79	17	100.0	10	1	AAAP40095 FMDV VP1
80	17	100.0	10	2	AAW41760 Colony st
81	17	100.0	10	2	AAW41760 Colony st
82	17	100.0	10	4	AAW41760 Colony st
83	17	100.0	10	4	AAW41760 Colony st
84	17	100.0	10	4	AAW41760 Colony st
85	17	100.0	10	4	AAW41760 Colony st
86	17	100.0	10	5	ABG65740 Plant ICK
87	17	100.0	10	5	ABG32275 Lysosyme
88	17	100.0	10	6	ABR09083 Human can
89	17	100.0	10	6	ABR09911 Human can
90	17	100.0	10	6	ABR10271 Human can
91	17	100.0	10	6	ABR09101 Human can
92	17	100.0	10	6	ABR09547 Human can
93	17	100.0	10	6	ABR09902 Human can
94	17	100.0	10	6	ABR09270 Human can
95	17	100.0	10	6	ABR09914 Human can
96	17	100.0	10	6	ABR09899 Human can
97	17	100.0	10	6	ABR09475 Human can
98	17	100.0	10	6	ABR09695 Human can

See ID 13 1-5
with 1 repeat
with x (any aa)

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100	17	100.0	10	6	ABR09471	Human can
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102	17	100.0	10	6	ABR09764	Human can
103	17	100.0	10	6	ABR09479	Human can
104	17	100.0	10	6	ABR09509	Human can
105	17	100.0	10	6	ABR10312	Human can
106	17	100.0	10	6	ABR09104	Human can
107	17	100.0	10	6	ABR09119	Human can
108	17	100.0	10	6	ABR09874	Human can
109	17	100.0	10	6	ABR09091	Human can
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111	17	100.0	10	6	ABR10103	Human can
112	17	100.0	10	6	ABR09275	Human can
113	17	100.0	10	6	ABR09270	Human can
114	17	100.0	10	6	ABR10125	Human can
115	17	100.0	10	6	ABR10311	Human can
116	17	100.0	10	6	ABR10316	Human can
117	17	100.0	10	6	ABR09282	Human can
118	17	100.0	10	6	ABR09693	Human can
119	17	100.0	10	6	ABR10068	Human can
120	17	100.0	10	6	ABR09284	Human can
121	17	100.0	10	6	ABR09903	Human can
122	17	100.0	10	6	ABR10100	Human can
123	17	100.0	10	6	ABR09103	Human can
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127	17	100.0	10	6	ABR10109	Human can
128	17	100.0	10	6	ABR10291	Human can
129	17	100.0	10	6	ABR10317	Human can
130	17	100.0	10	7	ADD15106	Peptide s
131	17	100.0	10	7	ADD23764	Breast ca
132	17	100.0	10	7	ADK24039	Human 98P
133	17	100.0	10	7	ADK24048	Human 98P
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138	17	100.0	11	2	AAE08092	Antifreeze
139	17	100.0	11	3	AAE69933	Human cyc
140	17	100.0	11	5	ABG31566	Lysozyme
141	17	100.0	11	5	AAU82656	Bp protei
142	17	100.0	11	5	AAU82657	Bp protei
143	17	100.0	11	6	AAE31824	Androgen
144	17	100.0	11	7	ADD15091	Peptide s
145	17	100.0	11	7	ADD15103	Peptide s
146	17	100.0	11	7	ADD15020	Peptide s
147	17	100.0	11	7	ADD15035	Peptide s
148	17	100.0	11	7	ADD15109	Peptide s
149	17	100.0	11	7	ADM09044	Canine im
150	17	100.0	11	8	ADK15579	Membrane
151	17	100.0	11	8	ADK17319	Human OCT
152	17	100.0	12	2	AAE67199	Bovine gl
153	17	100.0	12	2	AAE86663	GGF II tr
154	17	100.0	12	3	AAE29166	Peptide #
155	17	100.0	12	3	AAE29165	Peptide #
156	17	100.0	12	3	AAE81974	ORF encod
157	17	100.0	13	2	AAE97161	Conantoki
158	17	100.0	13	2	AAE05004	Tumour an
159	17	100.0	13	3	AAE99239	HLA class
160	17	100.0	13	6	AAE35589	Trojan an
161	17	100.0	13	6	ABU09119	Human Mad
162	17	100.0	13	6	ABU09121	Human Mad
163	17	100.0	13	7	ADC82726	CDR regio
164	17	100.0	13	7	ADFI1998	Mycobacte
165	17	100.0	13	8	ADK65093	PPIC-inte
166	17	100.0	13	8	ADM31945	A-A' beta
167	17	100.0	13	8	ADN64954	HLA bindi
168	17	100.0	13	8	ADO24026	HBV epito
169	17	100.0	14	1	AAE83237	Epstein-B
170	17	100.0	14	2	AAE32947	Mastopara
171	17	100.0	14	2	AAE32963	Mastopara
172	17	100.0	14	3	AAE99243	HLA class
173	17	100.0	14	4	AAE98274	Human pep
174	17	100.0	14	4	AAE98023	Human pep
175	17	100.0	14	6	ABR82573	BID alpha
176	17	100.0	14	6	ABR82574	BID alpha
177	17	100.0	14	6	ABR82572	BID alpha
178	17	100.0	14	7	ABW74394	DNA clone
179	17	100.0	14	8	ADK01533	Hepatitis
180	17	100.0	15	2	AAE56467	C-termina
181	17	100.0	15	2	AAE56467	B. mori s
182	17	100.0	15	2	AAW32854	Mastopara
183	17	100.0	15	2	AAW73726	M. tuberc
184	17	100.0	15	2	AAW73727	M. tuberc
185	17	100.0	15	2	AAW87843	Human Bcl
186	17	100.0	15	2	AAW73837	M. tuberc
187	17	100.0	15	2	AAW73836	M. tuberc
188	17	100.0	15	3	AAE94596	Mycobacte
189	17	100.0	15	3	AAE29738	Phage dis
190	17	100.0	15	3	ABE10822	Expressio
191	17	100.0	15	3	ABE10823	Expressio
192	17	100.0	15	4	AAE98975	Vaccine r
193	17	100.0	15	4	AAU10758	LEPB pep
194	17	100.0	15	4	AAU08191	Mycobacte
195	17	100.0	15	4	AAU08192	Mycobacte
196	17	100.0	15	4	AAE74160	BCL2 BHL
197	17	100.0	15	5	ABG30957	Mycobacte
198	17	100.0	15	5	ABG30958	Mycobacte
199	17	100.0	15	6	ABR32580	Human can
200	17	100.0	15	6	ABR32684	Human can

ALIGNMENTS

RESULT 1

ID	AAE20126	standard; peptide; 6 AA.
XX	AAE20126;	
AC	AAE20126;	
DT	18-JUN-2002	(first entry)
XX	Human TRIP leucine zipper peptide #1.	
DE	Human; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;	
XX	TRAF interacting protein; TRIP; cell activation; cell proliferation;	
KW	cell death; therapy; cytostatic; leucine zipper.	
XX	Homo sapiens.	
OS	US6346605-B1.	
EN	US6346605-B1.	
PD	12-FEB-2002.	
XX	31-MAR-1998;	98US-00052089.
PF	01-APR-1997;	97US-0042293P.
XX	07-APR-1997;	97US-0042747P.
PR	(UVRQ) UNIV ROCKEFELLER.	
XX	Lee SY, Choi Y;	
XX	WPI; 2002-225005/28.	
XX	New tumor necrosis factor receptor associated factor interacting protein,	
XX	useful for inhibiting NF-kappa B activation, and for modulating signals,	
XX	responsible for cell activation, cell proliferation and cell death.	
XX	Example 2; Fig 2E; 37pp; English.	
XX	The present invention relates to a tumour necrosis factor (TNF) receptor	
CC	associated factor (TRAF) interacting protein (TRIP), which is a regulator	

101	17	100.0	25	1	US-08-029-402-5	Sequence 5, Appli	174	17	100.0	39	3	US-09-238-303-13	Sequence 13, Appl
102	17	100.0	25	1	US-08-279-996-6	Sequence 6, Appli	175	17	100.0	39	3	US-09-315-304B-1457	Sequence 1457, Ap
103	17	100.0	25	1	US-08-934-741A-23	Sequence 23, Appl	176	17	100.0	39	4	US-09-104-337A-52	Sequence 52, Appl
104	17	100.0	25	6	5169933-42	Patent No. 5169933	177	17	100.0	39	4	US-09-946-239-13	Sequence 13, Appl
105	17	100.0	25	6	5248606-44	Patent No. 5248606	178	17	100.0	39	4	US-09-515-965A-1457	Sequence 1457, Ap
106	17	100.0	26	1	US-08-029-402-7	Sequence 7, Appli	179	17	100.0	39	4	US-09-350-641C-1457	Sequence 1457, Ap
107	17	100.0	26	1	US-08-029-402-9	Sequence 9, Appli	180	17	100.0	39	4	US-09-350-841A-1457	Sequence 1457, Ap
108	17	100.0	26	3	US-08-464-496-21	Sequence 11, Appl	181	17	100.0	40	1	US-08-279-058B-36	Sequence 26, Appl
109	17	100.0	26	3	US-08-197-484-115	Sequence 21, Appl	182	17	100.0	40	1	US-08-279-058B-33	Sequence 33, Appl
110	17	100.0	26	5	PCF-US92-07218-21	Sequence 115, Appl	183	17	100.0	40	3	US-09-154-083-16	Sequence 16, Appl
111	17	100.0	26	5	PCF-US95-02121-115	Sequence 115, Appl	184	17	100.0	40	4	US-08-828-323-26	Sequence 26, Appl
112	17	100.0	27	2	US-08-967-999-2	Sequence 3, Appli	185	17	100.0	40	4	US-08-828-323-33	Sequence 33, Appl
113	17	100.0	27	2	US-08-967-999-3	Sequence 3, Appli	186	17	100.0	40	4	US-09-461-325-315	Sequence 315, App
114	17	100.0	28	1	US-08-664-449-37	Sequence 37, Appl	187	17	100.0	40	4	US-10-012-542-315	Sequence 315, App
115	17	100.0	28	3	US-09-082-279B-1029	Sequence 1029, Ap	188	17	100.0	40	4	US-10-115-123-315	Sequence 315, App
116	17	100.0	28	3	US-09-315-304B-1029	Sequence 1029, Ap	189	17	100.0	41	4	US-08-469-260A-426	Sequence 426, App
117	17	100.0	28	4	US-09-834-784-1029	Sequence 1029, Ap	190	17	100.0	41	4	US-08-488-446-426	Sequence 426, App
118	17	100.0	28	4	US-09-515-965A-1029	Sequence 1029, Ap	191	17	100.0	41	4	US-08-467-344A-426	Sequence 426, App
119	17	100.0	28	4	US-09-350-641C-1029	Sequence 1029, Ap	192	17	100.0	41	4	US-09-270-767-45235	Sequence 45235, A
120	17	100.0	28	4	US-09-350-841A-1029	Sequence 1029, Ap	193	17	100.0	41	4	US-08-424-550B-426	Sequence 426, App
121	17	100.0	28	4	US-09-070-630-9	Sequence 9, Appli	194	17	100.0	42	1	US-08-664-449-39	Sequence 39, Appl
122	17	100.0	28	4	US-09-288-719B-21	Sequence 21, Appl	195	17	100.0	42	1	US-10-067-422-29	Sequence 29, Appl
123	17	100.0	29	1	US-08-029-402-19	Sequence 19, Appl	196	17	100.0	43	2	US-08-347-563A-12	Sequence 12, Appl
124	17	100.0	29	2	US-08-799-825-6	Sequence 6, Appli	197	17	100.0	43	3	US-08-485-942A-12	Sequence 12, Appl
125	17	100.0	29	3	US-09-280-068-6	Sequence 6, Appli	198	17	100.0	43	3	US-08-488-214A-12	Sequence 12, Appl
126	17	100.0	29	4	US-09-481-593-2	Sequence 2, Appli	199	17	100.0	43	3	US-08-488-208A-12	Sequence 12, Appl
127	17	100.0	30	2	US-08-716-317-16	Sequence 16, Appl	200	17	100.0	43	3	US-08-483-211A-12	Sequence 12, Appl
128	17	100.0	30	3	US-08-951-742-22	Sequence 22, Appl							
129	17	100.0	30	3	US-09-912-935-30	Sequence 30, Appl							
130	17	100.0	31	1	US-08-190-802A-232	Sequence 232, App							
131	17	100.0	31	3	US-08-477-346-232	Sequence 232, App							
132	17	100.0	31	3	US-08-473-089-232	Sequence 232, App							
133	17	100.0	31	4	US-08-487-072A-232	Sequence 232, App							
134	17	100.0	31	4	US-09-270-767-57895	Sequence 57895, A							
135	17	100.0	32	2	US-08-716-317-21	Sequence 21, Appl							
136	17	100.0	32	3	US-09-053-197A-68	Sequence 68, Appl							
137	17	100.0	32	3	US-09-085-761A-73	Sequence 73, Appl							
138	17	100.0	33	4	US-10-083-889-11	Sequence 11, Appl							
139	17	100.0	33	4	US-09-500-747-19	Sequence 19, Appl							
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141	17	100.0	34	1	US-07-773-098-6	Sequence 6, Appli							
142	17	100.0	34	2	US-08-716-317-26	Sequence 26, Appl							
143	17	100.0	34	2	US-08-934-741A-3	Sequence 3, Appli							
144	17	100.0	34	4	US-09-534-811-11	Sequence 11, Appl							
145	17	100.0	34	4	US-09-500-747-14	Sequence 14, Appl							
146	17	100.0	35	1	US-08-560-727-1	Sequence 1, Appli							
147	17	100.0	35	2	US-08-938-975-3	Sequence 3, Appli							
148	17	100.0	35	3	US-09-082-279B-717	Sequence 717, App							
149	17	100.0	35	3	US-09-315-304B-717	Sequence 717, App							
150	17	100.0	35	3	US-09-321-399-3	Sequence 3, Appli							
151	17	100.0	35	4	US-09-043-816E-44	Sequence 44, Appl							
152	17	100.0	35	4	US-09-323-379-3	Sequence 3, Appli							
153	17	100.0	35	4	US-09-834-784-717	Sequence 717, App							
154	17	100.0	35	4	US-09-515-965A-717	Sequence 717, App							
155	17	100.0	35	4	US-09-350-641C-717	Sequence 717, App							
156	17	100.0	35	4	US-09-270-767-61709	Sequence 61709, A							
157	17	100.0	35	4	US-09-350-841A-717	Sequence 717, App							
158	17	100.0	36	3	US-09-082-279B-751	Sequence 751, App							
159	17	100.0	36	3	US-09-315-304B-751	Sequence 751, App							
160	17	100.0	36	4	US-09-834-784-751	Sequence 751, App							
161	17	100.0	36	4	US-09-515-965A-751	Sequence 751, App							
162	17	100.0	36	4	US-09-897-956-5	Sequence 5, Appli							
163	17	100.0	36	4	US-09-350-641C-751	Sequence 751, App							
164	17	100.0	36	4	US-09-350-841A-751	Sequence 751, App							
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166	17	100.0	38	1	US-08-451-472-11	Sequence 11, Appl							
167	17	100.0	38	1	US-08-451-472-40	Sequence 40, Appl							
168	17	100.0	38	1	US-08-451-472-56	Sequence 56, Appl							
169	17	100.0	38	2	US-08-662-227-36	Sequence 36, Appl							
170	17	100.0	38	3	US-08-460-576-5	Sequence 5, Appli							
171	17	100.0	38	3	US-09-017-947-36	Sequence 36, Appl							
172	17	100.0	38	4	US-09-925-442-36	Sequence 36, Appl							
173	17	100.0	39	2	US-08-350-260A-52	Sequence 52, Appl							

RESULT 1

US-09-330-970-24

; Sequence 24, Application US/09330970

; Patent No. 6146876

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; APPLICANT: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide

; FILE REFERENCE: 5800-28

; CURRENT APPLICATION NUMBER: US/09/330,970

; CURRENT FILING DATE: 1999-06-11

; EARLIER APPLICATION NUMBER: 09/277,423

; EARLIER FILING DATE: 1999-03-26

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 24

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-330-970-24

Query Match 100.0%; Score 17; DB 3; Length 6;

Best Local Similarity 80.0%; Pred. No. 3.8e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XLAAX 5

Db 2 LLAAA 6

RESULT 2

US-09-330-970-38

; Sequence 38, Application US/09330970

; Patent No. 6146876

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; APPLICANT: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 08:05:22 ; Search time 139 Seconds
 (without alignments)
 12.759 Million cell updates/sec

Title: HOLLY-13
 Perfect score: 17
 Sequence: 1 xlaaa 5

Scoring table: BLOSUM62DX
 Gapop 10.0 , Gapext 0.5

Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 200 summaries

Database : Published Applications AA:*

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 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	100.0	7	16	US-10-363-204-242
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6	17	100.0	8	9	US-09-802-077-58
7	17	100.0	8	9	US-09-802-096-25
8	17	100.0	8	9	US-09-802-096-58
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 Sequence 2843, Ap
 Sequence 3286, Ap
 Sequence 8, Appli
 Sequence 1, Appli
 Sequence 2, Appli
 Sequence 89, Appl
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 Sequence 164, App
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 Sequence 16, Appl
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					US-10-424-599-214715	Sequence 214715,	Sequence 214715,
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ALIGNMENTS

RESULT 1

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; Patent No. US2002017231A1
; GENERAL INFORMATION:
; APPLICANT: Staunton et al.
; TITLE OF INVENTION: Leupaxin Materials and Methods
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/211,424A
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 23
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified human
; OTHER INFORMATION: sequence
US-09-211-424-23

Query Match 100.0%; Score 17; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 X1AAA 5

Db 1 N1AAA 5

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:59:16 ; Search time 16 Seconds

(Without alignments)
30.068 Million cell updates/sec

Title: HOLLY-13

Perfect score: 17

Sequence: 1 xlaaa 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

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2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	100.0	23	B37843	vrg 18 protein - B
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6	17	100.0	28	S21278	glutathione transf
7	17	100.0	29	C54037	splicing regulator
8	17	100.0	30	I55427	aspartate transami
9	17	100.0	30	S19609	glucosylglicosacchari
10	17	100.0	33	FDPI5G	antifreeze protein
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22	17	100.0	43	S24180	histone H1.a, test
23	17	100.0	43	H81142	hypothetical prote
24	17	100.0	44	T03953	hypothetical prote
25	17	100.0	45	A05163	antifreeze protein
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29	17	100.0	47	AB2489	hypothetical prote

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bacteriochlorophyl
photosystem ii pro
basic helix-loop-h
hypothetical prote
glutathione transf
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probable regulator
light-harvesting p
ribosomal protein
light-harvesting p
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112	17	100.0	79	2	A13344	protein translocas
113	17	100.0	80	2	S34219	acclimation protei
114	17	100.0	81	1	LVYCA	H+-transporting tw
115	17	100.0	81	1	C31090	H+-transporting tw
116	17	100.0	81	2	A11807	ATP synthase chain
117	17	100.0	81	2	G87600	hypothetical prote
118	17	100.0	81	2	F75409	hypothetical prote
119	17	100.0	81	2	S20031	hypothetical prote
120	17	100.0	81	2	B70966	hypothetical prote
121	17	100.0	81	2	T10320	hypothetical prote
122	17	100.0	81	2	B95401	hypothetical prote
123	17	100.0	82	2	S36961	H+-transporting tw
124	17	100.0	82	2	E70972	probable enoyl-coA
125	17	100.0	82	2	A47482	pilin-like coloniz
126	17	100.0	82	2	A97840	hypothetical prote
127	17	100.0	82	2	B95846	hypothetical prote
128	17	100.0	83	2	T34904	hypothetical prote
129	17	100.0	83	2	C95402	hypothetical prote
130	17	100.0	84	1	Q9EC7	hypothetical prote
131	17	100.0	84	2	G70787	hypothetical prote
132	17	100.0	84	2	T04475	probable acclimat
133	17	100.0	85	1	IHTFER	high potential iro
134	17	100.0	85	2	S48010	Ip5 protein - phag
135	17	100.0	85	2	G70824	hypothetical prote
136	17	100.0	85	2	D69268	hypothetical prote
137	17	100.0	85	2	AC3416	hypothetical cytos
138	17	100.0	86	2	AG2402	photosystem I chai
139	17	100.0	86	2	B96709	hypothetical prote
140	17	100.0	86	2	S32922	trbE protein - Esc
141	17	100.0	86	2	AC3459	hypothetical prote
142	17	100.0	87	2	T29724	hypothetical prote
143	17	100.0	87	2	AC2723	hypothetical prote
144	17	100.0	88	2	S25078	acyl carrier prote
145	17	100.0	88	2	S16851	BLN14 protein - ba
146	17	100.0	89	2	I68553	cell surface glyco
147	17	100.0	89	2	S24178	histone H1.d, hepa
148	17	100.0	89	2	A81013	sugar transport Pr
149	17	100.0	89	2	C84242	hypothetical prote
150	17	100.0	89	2	T45015	hypothetical prote
151	17	100.0	89	2	S31949	penicillin-binding
152	17	100.0	89	2	S56690	hypothetical prote
153	17	100.0	89	2	A53238	phenomycin - Stre
154	17	100.0	89	2	A22287	hypothetical prote
155	17	100.0	90	2	F82976	probable DNA-bind
156	17	100.0	90	2	E81777	probable periplasm
157	17	100.0	91	1	S09524	mercuric resistanc
158	17	100.0	91	1	RGBHD	mercuric resistanc
159	17	100.0	91	2	T08131	oleosin-like prote
160	17	100.0	91	2	T45346	hypothetical prote
161	17	100.0	91	2	D70780	hypothetical prote
162	17	100.0	92	1	R1PGS	somatostatin I pre
163	17	100.0	92	2	T08129	oleosin-like prote
164	17	100.0	92	2	B69150	conserved hypothet
165	17	100.0	92	2	H84264	hypothetical prote
166	17	100.0	92	2	S39089	cell wall mamopro
167	17	100.0	93	2	D87257	conserved hypothet
168	17	100.0	93	2	B36942	fpbB protein - Pae
169	17	100.0	93	2	C82440	hypothetical prote
170	17	100.0	93	2	AF3485	hypothetical prote
171	17	100.0	94	1	COSJS	lg2 protein - brac
172	17	100.0	94	2	E84281	hypothetical prote
173	17	100.0	94	2	F31844	spdA protein - Str
174	17	100.0	94	2	T03285	anther-specific pr
175	17	100.0	94	2	C98239	hypothetical prote

ALIGNMENTS

RESULT 1

A43848
 cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
 C:Species: Staphylococcus aureus
 C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A43848
 R:Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
 Infect. Immun. 60, 899-906, 1992
 A:Title: Binding of heparan sulfate to Staphylococcus aureus.
 A:Reference number: A43848; MUID:92176005; PMID:1541563
 A:Accession: A43848
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <LIA>
 A:Cross-references: UNIPROT:Q9RSM1
 A>Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 100.0%; Score 17; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XLAAA 5
 :|||
 DB 5 WLAAG 9

RESULT 2

A38929
 glutathione peroxidase (EC 1.11.1.9) - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 A:Reference number: S21712; MUID:92231574; PMID:1567207
 C:Accession: A38929
 R:Gottina, P.; Dyal, D.; Crews, B.
 Arch. Biochem. Biophys. 294, 511-518, 1992
 A:Title: Selenium-dependent glutathione peroxidases from ovine and bovine erythrocytes
 A:Reference number: S21712; MUID:92231574; PMID:1567207
 A:Accession: A38929
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <GET>
 A:Cross-references: UNIPROT:Q7M355
 C:Superfamily: glutathione peroxidase
 C:Keywords: oxidoreductase

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2004, 07:58:41 ; Search time 62 Seconds
(without alignments)

46.401 Million cell updates/sec

Title: HOLLY-13

Perfect score: 17

Sequence: 1 xlaaa 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 200 summaries

Database : UniProt.02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	9	2	Q9R5M1
2	17	100.0	10	2	Q94I19
3	17	100.0	13	2	Q7M355
4	17	100.0	15	2	Q9FYV6
5	17	100.0	16	2	Q9JHM3
6	17	100.0	17	2	Q7JMY3
7	17	100.0	17	2	Q7YK33
8	17	100.0	21	2	Q9UCJ6
9	17	100.0	21	2	Q9UCJ6
10	17	100.0	22	2	Q94I33
11	17	100.0	22	2	Q7L8R0
12	17	100.0	22	2	Caa22266
13	17	100.0	23	2	Q8MF13
14	17	100.0	23	2	Q8MF15
15	17	100.0	23	2	Q8MF17
16	17	100.0	23	2	Q8MF19
17	17	100.0	23	2	Q8MFV1
18	17	100.0	23	2	Q8MFV3
19	17	100.0	23	2	Q8MFV5
20	17	100.0	23	2	Q8MFV7
21	17	100.0	23	2	Q8MFV9
22	17	100.0	23	2	Q8MFK1
23	17	100.0	23	2	Q8MFK3
24	17	100.0	23	2	Q8MFK5
25	17	100.0	23	2	Q04274
26	17	100.0	23	2	Q84F40
27	17	100.0	24	2	Q8R2H8
28	17	100.0	27	1	PSBY_FUCVE
29	17	100.0	27	2	Q6V100
30	17	100.0	27	2	Q80WY7
31	17	100.0	27	2	AAQ55837
32	17	100.0	28	2	Q8IZL0
33	17	100.0	28	2	Q8IZL0
34	17	100.0	28	2	Q8IZL0
35	17	100.0	28	2	Q8IZL0
36	17	100.0	28	2	Q8IZL0
37	17	100.0	28	2	Q8IZL0
38	17	100.0	28	2	Q8IZL0
39	17	100.0	28	2	Q8IZL0
40	17	100.0	28	2	Q8IZL0
41	17	100.0	28	2	Q8IZL0
42	17	100.0	28	2	Q8IZL0
43	17	100.0	28	2	Q8IZL0
44	17	100.0	28	2	Q8IZL0
45	17	100.0	28	2	Q8IZL0
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47	17	100.0	28	2	Q8IZL0
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49	17	100.0	28	2	Q8IZL0
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51	17	100.0	28	2	Q8IZL0
52	17	100.0	28	2	Q8IZL0
53	17	100.0	28	2	Q8IZL0
54	17	100.0	28	2	Q8IZL0
55	17	100.0	28	2	Q8IZL0
56	17	100.0	28	2	Q8IZL0
57	17	100.0	28	2	Q8IZL0
58	17	100.0	28	2	Q8IZL0
59	17	100.0	28	2	Q8IZL0
60	17	100.0	28	2	Q8IZL0
61	17	100.0	28	2	Q8IZL0
62	17	100.0	28	2	Q8IZL0
63	17	100.0	28	2	Q8IZL0
64	17	100.0	28	2	Q8IZL0
65	17	100.0	28	2	Q8IZL0
66	17	100.0	28	2	Q8IZL0
67	17	100.0	28	2	Q8IZL0
68	17	100.0	28	2	Q8IZL0
69	17	100.0	28	2	Q8IZL0
70	17	100.0	28	2	Q8IZL0
71	17	100.0	28	2	Q8IZL0
72	17	100.0	28	2	Q8IZL0
73	17	100.0	28	2	Q8IZL0
74	17	100.0	28	2	Q8IZL0
75	17	100.0	28	2	Q8IZL0
76	17	100.0	28	2	Q8IZL0
77	17	100.0	28	2	Q8IZL0
78	17	100.0	28	2	Q8IZL0
79	17	100.0	28	2	Q8IZL0
80	17	100.0	28	2	Q8IZL0
81	17	100.0	28	2	Q8IZL0
82	17	100.0	28	2	Q8IZL0
83	17	100.0	28	2	Q8IZL0
84	17	100.0	28	2	Q8IZL0
85	17	100.0	28	2	Q8IZL0
86	17	100.0	28	2	Q8IZL0
87	17	100.0	28	2	Q8IZL0
88	17	100.0	28	2	Q8IZL0
89	17	100.0	28	2	Q8IZL0
90	17	100.0	28	2	Q8IZL0
91	17	100.0	28	2	Q8IZL0
92	17	100.0	28	2	Q8IZL0
93	17	100.0	28	2	Q8IZL0
94	17	100.0	28	2	Q8IZL0
95	17	100.0	28	2	Q8IZL0
96	17	100.0	28	2	Q8IZL0
97	17	100.0	28	2	Q8IZL0
98	17	100.0	28	2	Q8IZL0
99	17	100.0	28	2	Q8IZL0
100	17	100.0	28	2	Q8IZL0
101	17	100.0	28	2	Q8IZL0
102	17	100.0	28	2	Q8IZL0
103	17	100.0	28	2	Q8IZL0
104	17	100.0	28	2	Q8IZL0

Q71kp5 spirogyra m
Q79CG0 neisseria g
Q7vel4 mycobacteri
Q6mx19 mycobacteri
Q9qvc9 rattus sp.
Aab63319 neisseria
AaQ05912 spirogyra
CaE55539 mycobacte
Q85fp9 cyanidiosch
Q9jlg6 rattus norv
Aaf63713 homo sapi
Q9urb6 acromonium
Q9bwz3 homo sapien
Q6lbu2 triticum ae
CaA31327 triticum
P23372 diptoptera
Q9fuq2 zea mays (s
Q80rg7 newcastle d
Q80RG7
Q96RX4
Q96RX4 homo sapien
Q3mv20 arabidopsis
Q9g284 polygonum c
Q9g265 polygonum c
Q9g266 polygonum c
Q9gfg7 polygonum w
Q9gfi3 polygonum s
Q9fe80 zea diplope
Q9fe81 zea mays (s
Q9fe82 zea mays (s
Q9fup8 zea luxuria
Q9fup9 zea luxuria
Q9fuq0 zea luxuria
Q9fuq1 zea mays (s
Q9fuq3 zea mays (s
Q9fuq4 zea mays (s
Q9fuq5 zea mays (m
Q72f90 desulfovibr
Aas94807 desulfovi
P04367 myoxocephal
P20421 myoxocephal
Q7z2m7 homo sapien
Q6xqj3 pseudomonas
Aap49281 pseudomon
Aap1g9 cyanidium c
P51206 porphyra pu
Q7jmv4 anopheles g
Q9kmr8 vibrio chol
Q78433 guillardia
Q9hrw1 halobacteri
Q8lid9 vibrio angu
Q98a46 rhizobium l
Q7shl3 neurospora
Q7si50 neurospora
Q939w1 aeromonas s
Q9jue4 neisseria m
Q8viu8 mycobacteri
P20617 myoxocephal
P94416 bacillus su
Q6tnz4 rattus norv
Q6dl79 bacillus mo
Q6dl81 bacillus su
Q9tnz5 rattus norv
Q53456 streptomyce
Q8a790 caulobacter
Q7X5B5 synecococc
Q7M0F6 mesocricetu
Q69019 human herpe
Q9dfi8 myoxocephal
Q7ljq2 fusarium ps
Q7ljt0 fusarium cu
Q7ljts fusarium lu
Q7lp62 gibberella
Q8nje8 fusarium ce
Q9cia7 fusarium ce

105	17	100.0	43	2	Q9C1B4	Q9C1B4 fusarium sp
106	17	100.0	43	2	Q6AS2	Q6AS2 equus caball
107	17	100.0	43	2	Q9TNZ6	Q9TNZ6 rattus norv
108	17	100.0	43	2	Q9L7U00	Q9L7U00 synechococ
109	17	100.0	43	2	Q9JZS3	Q9JZS3 neisseria m
110	17	100.0	43	2	Q8XW38	Q8XW38 ralstonia s
111	17	100.0	43	2	Q6EWA2	Q6EWA2 human calci
112	17	100.0	44	2	Q9S562	Q9S562 rattus norv
113	17	100.0	44	2	Q24577	Q24577 zea mays (m
114	17	100.0	44	2	Q9L7E4	Q9L7E4 synechococ
115	17	100.0	44	2	Q7UPL2	Q7UPL2 rhodospirill
116	17	100.0	44	2	Q8E288	Q8E288 leptospira
117	17	100.0	45	1	ANP8_MYOSC	P04368 myxocephal
118	17	100.0	45	2	Q7L6R4	Q7L6R4 mycobacteri
119	17	100.0	45	2	Q6X937	Q6X937 proteus mir
120	17	100.0	45	2	Q7H303	Q7H303 paracoccus
121	17	100.0	45	2	Q6LEL2	Q6LEL2 gallus gall
122	17	100.0	45	2	AAQ12088	AAQ12088 mycobacte
123	17	100.0	45	2	AAQ12022	AAQ12022 gallus ga
124	17	100.0	45	2	AAQ76377	AAQ76377 proteus m
125	17	100.0	46	2	Q92ID2	Q92ID2 mycoplasma
126	17	100.0	46	2	Q7MUH0	Q7MUH0 porphyromon
127	17	100.0	46	2	Q8FUU7	Q8FUU7 brucella su
128	17	100.0	46	2	Q8Z7T3	Q8Z7T3 salmonella
129	17	100.0	47	1	RECA_PSEST	Q07809 pseudomonas
130	17	100.0	47	2	Q7OXV1	Q7OXV1 giardia lam
131	17	100.0	47	2	Q41781	Q41781 zea mays (m
132	17	100.0	47	2	Q9X3P9	Q9X3P9 prochloroco
133	17	100.0	47	2	Q8YL45	Q8YL45 anabaena sp
134	17	100.0	47	2	Q90329	Q90329 coturnix co
135	17	100.0	47	2	Q90774	Q90774 gallus gall
136	17	100.0	48	1	CSMA_CHLIT	P15524 chlorobium
137	17	100.0	48	1	CSMA_PROAE	P15528 prosthecoch
138	17	100.0	48	1	RBL_FINPS	P81080 pinus pinas
139	17	100.0	48	2	Q8WR24	Q8WR24 anopheles g
140	17	100.0	48	2	Q05461	Q05461 zea mays (m
141	17	100.0	48	2	Q02801	Q02801 streptomyce
142	17	100.0	48	2	Q46040	Q46040 cellulomona
143	17	100.0	48	2	Q88JK5	Q88JK5 pseudomonas
144	17	100.0	48	2	Q8CKM0	Q8CKM0 yersinia pe
145	17	100.0	48	2	Q8G2K2	Q8G2K2 brucella su
146	17	100.0	48	2	Q918B5	Q918B5 tetracodon n
147	17	100.0	49	2	Q7S4A4	Q7S4A4 neurospora
148	17	100.0	49	2	Q95SN2	Q95SN2 dirosophia
149	17	100.0	49	2	Q7WYV8	Q7WYV8 xanthomonas
150	17	100.0	49	2	Q92R21	Q92R21 rhizobium m
151	17	100.0	49	2	Q8VJ10	Q8VJ10 mycobacteri
152	17	100.0	49	2	Q8VJQ9	Q8VJQ9 mycobacteri
153	17	100.0	49	2	Q7M0B9	Q7M0B9 mus musculu
154	17	100.0	50	1	LHB2_RHOSH	P02952 rhodobacter
155	17	100.0	50	2	Q7PFV7	Q7PFV7 anopheles g
156	17	100.0	50	2	Q04724	Q04724 zea mays (m
157	17	100.0	50	2	Q9SM32	Q9SM32 triticum ae
158	17	100.0	50	2	Q9L7F4	Q9L7F4 synechococ
159	17	100.0	50	2	Q7VZM4	Q7VZM4 bordetella
160	17	100.0	50	2	Q7WM35	Q7WM35 bordetella
161	17	100.0	50	2	Q8VKL5	Q8VKL5 mycobacteri
162	17	100.0	50	2	Q71AA5	Q71AA5 mamestra co
163	17	100.0	50	2	Q8QLC7	Q8QLC7 mamestra co
164	17	100.0	50	2	AAQ11126	AAQ11126 mamestra
165	17	100.0	51	1	RL39_PYRAE	Q8ZTX6 pyrobaculum
166	17	100.0	51	2	Q8TBL2	Q8TBL2 homo sapien
167	17	100.0	51	2	Q8GVN9	Q8GVN9 oryza sativ
168	17	100.0	51	2	Q8LCJ2	Q8LCJ2 arabidopsis
169	17	100.0	51	2	Q9FP56	Q9FP56 oryza sativ
170	17	100.0	51	2	Q94LB1	Q94LB1 arabidopsis
171	17	100.0	51	2	Q9AJQ9	Q9AJQ9 vibrio fisc
172	17	100.0	51	2	Q7NYK6	Q7NYK6 chromobacte
173	17	100.0	51	2	Q7WBH3	Q7WBH3 bordetella
174	17	100.0	51	2	Q8VKP0	Q8VKP0 mycobacteri
175	17	100.0	51	2	Q8X220	Q8X220 escherichia
176	17	100.0	51	2	Q8YBX8	Q8YBX8 brucella me
177	17	100.0	51	2	Q800J8	Q800J8 pleocoglossu
178	17	100.0	51	2	Q8AH5	Q8AH5 pseudopleur
179	17	100.0	51	2	Q8I821	Q8I821 oncorhynch
180	17	100.0	51	2	Q9PSB5	Q9PSB5 oncorhynch
181	17	100.0	51	2	Q9PSB6	Q9PSB6 carassius a
182	17	100.0	51	2	Q9PSE7	Q9PSE7 carassius a
183	17	100.0	52	2	Q6MZF9	Q6MZF9 homo sapien
184	17	100.0	52	2	Q6ZAK4	Q6ZAK4 oryza sativ
185	17	100.0	52	2	Q8AH5	Q8AH5 rhizobium l
186	17	100.0	52	2	Q8XYS7	Q8XYS7 ralstonia s
187	17	100.0	52	2	Q7MSJ7	Q7MSJ7 fowl adenov
188	17	100.0	52	2	CAE46080	CAE46080 homo sapi
189	17	100.0	52	2	BAC99634	BAC99634 oryza sat
190	17	100.0	53	2	Q28023	Q28023 bos taurus
191	17	100.0	53	2	Q28551	Q28551 ovis aries
192	17	100.0	53	2	Q8RZF2	Q8RZF2 oryza sativ
193	17	100.0	53	2	Q79F45	Q79F45 rhodobacter
194	17	100.0	53	2	Q8EX6	Q8EX6 rhizobium l
195	17	100.0	53	2	Q8VJ18	Q8VJ18 mycobacteri
196	17	100.0	53	2	Q8X2S0	Q8X2S0 escherichia
197	17	100.0	53	2	Q8EP65	Q8EP65 mus musculu
198	17	100.0	53	2	Q11370	Q11370 molluscum c
199	17	100.0	54	2	Q853H8	Q853H8 mycobacteri
200	17	100.0	54	2	Q9XC9	Q9XC9 streptomyce

ALIGNMENTS

RESULT 1

Q9R5M1 PRELIMINARY; PRT; 9 AA.
 ID Q9R5M1
 AC Q9R5M1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP MEDLINE=92176005; PubMed=1541563;
 RA Liang O.D., Ascencio F., Francon L.A., Wadstrom T.;
 RT "Binding of heparan sulfate to Staphylococcus aureus";
 RL Infect. Immun. 60:899-906(1992).
 DR PIR; A43848; A43848.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 990 MW; 2289DDD7337861B3 CRC64;

Query Match 100.0%; Score 17; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XLA 5
 Db 5 WLA 9

RESULT 2

Q94II9 PRELIMINARY; PRT; 10 AA.
 ID Q94II9
 AC Q94II9
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Anthocyanin regulator R-sc protein (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]